

SEQUENCE LISTING

<110> UEMURA, Hidetoshi
OKUI, Akira
KOMINAMI, Katsuya
YAMAGUCHI, Nozomi
MITSUI, Shinichi

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<140> 09/856,320

<141> 2001-05-21

<150> JP 10-347802

<151> 1998-11-20

<160> 41

<170> PatentIn version 3.1

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Met Gln

agg ttg agg tgg ctg cgg gac tgg aag tca tgc ggc aga ggt ctc aca 166
Arg Leu Arg Trp Leu Arg Asp Trp Lys Ser Ser Gly Arg Gly Leu Thr
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Ala Ala Lys Glu Pro Gly Ala Arg Ser Ser Pro Leu Gln Ala Met Arg
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att ctg cag tta atc ctg ctt gct ctg gca aca ggg ctt gta ggg gga 262
Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly Gly
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ctc	atc	gcc	ccc	aga	tgg	ctc	ctg	aca	gca	gcc	cac	tgc	ctc	aag	ccc	406	
Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala	Ala	His	Cys	Leu	Lys	Pro		
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cgc	tac	ata	gtt	cac	ctg	ggg	cag	cac	aac	ctc	cag	aag	gag	gag	ggc	454	
Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His	Asn	Leu	Gln	Lys	Glu	Glu	Gly		
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Cys	Glu	Gln		Arg	Thr	Ala	Thr	Glu	Ser	Phe	Pro	His	Pro	Gly	Phe		
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Asn	Asn	Ser	Leu	Pro	Asn	Lys	Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val		
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Lys	Met	Ala	Ser	Pro	Val	Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr		
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ctc	tcc	tca	cgc	tgt	gtc	act	gct	ggc	acc	agc	tgc	ctc	att	tcc	ggc	646	
Leu	Ser	Ser	Arg	Cys	Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly		
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Trp	Gly	Ser	Thr	Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg		
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Cys	Ala	Asn	Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr		
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Pro	Gly	Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly		
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Gly	Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn		
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cag	tct	ctt	caa	ggc	att	atc	tcc	tgg	ggc	cag	gat	ccg	tgt	gcg	atc	886	
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	Ile		
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acc	cga	aag	cct	ggt	gtc	tac	acg	aaa	gtc	tgc	aaa	tat	gtg	gac	tgg	934	
Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	Asp	Trp		
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Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn										
			225														
ccctccattt	ccacttggtg	tttgggttcct	gttcactctg	ttaataagaa	accctaagcc											1048	
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 -35 -30 -25

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val
 -20 -15 -10

Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser
 -5 -1 1 5 10

Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
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Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu
 30 35 40

Lys Pro Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu
 45 50 55

Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro
 60 65 70 75

Gly Phe Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met
 80 85 90

Leu Val Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro
 95 100 105

Leu Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile
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Ser Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr
 125 130 135

Leu Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn
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Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln
160 165 170

Glu Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
175 180 185

Cys Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys
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Met Arg Arg Leu
-45

aag agt gac tgg aaa tta tct aca gaa acc agg gaa cct ggc gcc cgc 162
Lys Ser Asp Trp Lys Leu Ser Thr Glu Thr Arg Glu Pro Gly Ala Arg
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cct gcc cta ctc cag gcc agg atg att ctc cga ctc att gca ctt gct 210
Pro Ala Leu Leu Gln Ala Arg Met Ile Leu Arg Leu Ile Ala Leu Ala
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ctg gta aca ggg cac gta ggg gga gag acg agg atc atc aag ggt tat 258
Leu Val Thr Gly His Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Tyr
-10 -5 -1 1 5

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Glu Cys Arg Pro His Ser Gln Pro Trp Gln Val Ala Leu Phe Gln Lys
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Thr Arg Leu Leu Cys Gly Ala Thr Leu Ile Ala Pro Lys Trp Leu Leu

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aca gca gcc cac tgc cgc aag ccc cat tac gtg atc ctc ctt gga gag			402
Thr Ala Ala His Cys Arg Lys Pro His Tyr Val Ile Leu Leu Gly Glu			
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cac aat cta gag aag aca gac ggc tgt gag cag agg cgg atg gcc act			450
His Asn Leu Glu Lys Thr Asp Gly Cys Glu Gln Arg Arg Met Ala Thr			
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gag tcc ttc ccc cac ccc gac ttc aac aac agc ctc ccc aac aaa gac			498
Glu Ser Phe Pro His Pro Asp Phe Asn Asn Ser Leu Pro Asn Lys Asp			
70	75	80	85
cac cgg aat gac ata atg ctt gtg aag atg tcg tct ccc gtc ttc ttt			546
His Arg Asn Asp Ile Met Leu Val Lys Met Ser Ser Pro Val Phe Phe			
90	95	100	
acc cga gct gtg cag cca ctc acc ctg tcc cca cac tgt gtc gct gca			594
Thr Arg Ala Val Gln Pro Leu Thr Leu Ser Pro His Cys Val Ala Ala			
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ggc acc agc tgc ctc att tct gga tgg ggc acc acg tcc agc ccc cag			642
Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Thr Thr Ser Ser Pro Gln			
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Leu Arg Leu Pro His Ser Leu Arg Cys Ala Asn Val Ser Ile Ile Glu			
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cac aag gag tgt gag aag gcc tac ccg ggc aac atc aca gac acc atg			738
His Lys Glu Cys Glu Lys Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met			
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ctg tgc gcc agt gtt cgg aaa gag ggc aag gac tcc tgt cag ggt gac			786
Leu Cys Ala Ser Val Arg Lys Glu Gly Lys Asp Ser Cys Gln Gly Asp			
170	175	180	
tct gga ggc ccc ctg gtc tgc aac gga tct ctt caa ggc atc atc tcc			834
Ser Gly Gly Pro Leu Val Cys Asn Gly Ser Leu Gln Gly Ile Ile Ser			
185	190	195	
tgg ggt cag gac cca tgt gcc gtc acc aga aag cct ggt gtc tat aca			882
Trp Gly Gln Asp Pro Cys Ala Val Thr Arg Lys Pro Gly Val Tyr Thr			
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aaa gtc tgc aaa tac ttt aac tgg atc cac gag gtt atg agg aac aat			930
Lys Val Cys Lys Tyr Phe Asn Trp Ile His Glu Val Met Arg Asn Asn			
215	220	225	
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tcttcattct gccctaagaa gtcctcagct gggaccctgg catgtactct ctccgaccca			1050
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cctgacttga actaaattgt gactctggac atgatcacca ctggttttgt ttgtttggtt			1170
gttttttgtt ttgttttgtt ttgttccag ctttgaagac agtccctggc atatcccagg			1230
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 -15 -10 -5 -1 1

Ile Lys Gly Tyr Glu Cys Arg Pro His Ser Gln Pro Trp Gln Val Ala
 5 10 15

Leu Phe Gln Lys Thr Arg Leu Leu Cys Gly Ala Thr Leu Ile Ala Pro
 20 25 30

Lys Trp Leu Leu Thr Ala Ala His Cys Arg Lys Pro His Tyr Val Ile
 35 40 45

Leu Leu Gly Glu His Asn Leu Glu Lys Thr Asp Gly Cys Glu Gln Arg
 50 55 60 65

Arg Met Ala Thr Glu Ser Phe Pro His Pro Asp Phe Asn Asn Ser Leu
 70 75 80

Pro Asn Lys Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ser Ser
 85 90 95

Pro Val Phe Phe Thr Arg Ala Val Gln Pro Leu Thr Leu Ser Pro His
 100 105 110

Cys Val Ala Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Thr Thr
 115 120 125

Ser Ser Pro Gln Leu Arg Leu Pro His Ser Leu Arg Cys Ala Asn Val
 130 135 140 145

Ser Ile Ile Glu His Lys Glu Cys Glu Lys Ala Tyr Pro Gly Asn Ile
 150 155 160

Thr Asp Thr Met Leu Cys Ala Ser Val Arg Lys Glu Gly Lys Asp Ser
 165 170 175

Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Ser Leu Gln
180 185 190

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Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln Pro
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Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala Thr
15 20 25

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Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys Pro
30 35 40 45

tgg gtg tca ctc acc tct ccc acc cat gtc tcc ccc gac ctt tcc tcc 296
Trp Val Ser Leu Thr Ser Pro Thr His Val Ser Pro Asp Leu Ser Ser
50 55 60

tcc aac tac tgt ctc tcc cac ctc agc cgc tac ata gtt cac ctg ggg 344
Ser Asn Tyr Cys Leu Ser His Leu Ser Arg Tyr Ile Val His Leu Gly
65 70 75

cag cac aac ctc cag aag gag gag ggc tgt gag cag acc cgg aca gcc	392
Gln His Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala	
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Thr Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys	
95 100 105	
gac cac cgc aat gac atc atg ctg gtg aag atg gca tcg cca gtc tcc	488
Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro Val Ser	
110 115 120 125	
atc acc tgg gct gtg cga ccc ctc acc ctc tcc tca cgc tgy gtc act	536
Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys Val Thr	
130 135 140	
gct ggc acc agc tgc ctc att tcc ggc tgg ggc agc acg tcc agc ccc	584
Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr Ser Ser Pro	
145 150 155	
cag tta cgc ctg cct cac acc ttg cga tgc gcc aac atc acc atc att	632
Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn Ile Thr Ile Ile	
160 165 170	
gag cac cag aag tgt gag aac gcc tac ccc ggc aac atc aca gac acc	680
Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly Asn Ile Thr Asp Thr	
175 180 185	
atg gtg tgt gcc agc gtg cag gaa ggg ggc aag gac tcc tgc cag ggt	728
Met Val Cys Ala Ser Val Gln Glu Gly Gly Lys Asp Ser Cys Gln Gly	
190 195 200 205	
gac tcc ggg ggc cct ctg gtc tgt aac cag tct ctt caa ggc att atc	776
Asp Ser Gly Gly Pro Leu Val Cys Asn Gln Ser Leu Gln Gly Ile Ile	
210 215 220	
tcc tgg ggc cag gat ccg tgt gcg atc acc cga aag cct ggt gtc tac	824
Ser Trp Gly Gln Asp Pro Cys Ala Ile Thr Arg Lys Pro Gly Val Tyr	
225 230 235	
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Thr Lys Val Cys Lys Tyr Val Asp Trp Ile Gln Glu Thr Met Lys Asn	
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Asn	
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Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu
 30 35 40

Lys Pro Trp Val Ser Leu Thr Ser Pro Thr His Val Ser Pro Asp Leu
 45 50 55

Ser Ser Ser Asn Tyr Cys Leu Ser His Leu Ser Arg Tyr Ile Val His
 60 65 70 75

Leu Gly Gln His Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg
 80 85 90

Thr Ala Thr Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro
 95 100 105

Asn Lys Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro
 110 115 120

Val Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys
 125 130 135

Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr Ser
 140 145 150 155

Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn Ile Thr
 160 165 170

Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly Asn Ile Thr
 175 180 185

Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly Lys Asp Ser Cys
 190 195 200

Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gln Ser Leu Gln Gly
 205 210 215

Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala Ile Thr Arg Lys Pro Gly
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Val Tyr Thr Lys Val Cys Lys Tyr Val Asp Trp Ile Gln Glu Thr Met
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Lys Asn Asn

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<213> Artificial Sequence

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<220>
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<210> 9
<211> 15
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<220>
<223> Designed oligonucleotide primer to amplify neurosin-encoding sequence

<400> 9
ttggtgcatg gcgga                                                            15

<210> 10
<211> 27
<212> DNA
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<220>
<223> Designed oligonucleotide primer to amplify neurosin-encoding sequence

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tcctcgagac ttggcctgaa tggtttt                                             27

<210> 11
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 <223> Designed oligonucleotide primer to amplify a portion of plasmid p
 SecTrypHis/Neurosin

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 <212> DNA
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 tgaagcttgc catggaccaa cttgtcatc 29

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 <210> 16
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 <400> 16
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 <400> 17
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 <210> 18
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 <400> 18
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 <210> 19
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as hBSSP6F2 for RACE f or human BSSP6 (forward)

 <400> 19
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 <210> 20
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer designated as hBSSP6F3 to amplify full-length human brain BSSP6-encoding mRNA (forward)

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<210> 21
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<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as hBSSP6F4 to amplify
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<210> 22
<211> 20
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<220>
<223> Designed oligonucleotide primer designated as hBSSP6F5 to amplify
        full-length human prostate BSSP6-encoding mRNA (forward)

<400> 22
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<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as hBSSP6R1 for RACE f
        or human BSSP6 (reverse)

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<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as hBSSP6R2 for RACE f
        or human BSSP6 (reverse)

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<210> 25
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as hBSSP6R3/P to ampli
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<210> 26
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<213> Artificial Sequence

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<223> Designed oligonucleotide primer designated as mBSSP6F1 for RACE f
      or mouse BSSP6 (forward)

<400> 26
cgacttcaac aacagcctcc                                     20

<210> 27
<211> 20
<212> DNA
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<220>
<223> Designated oligonucleotide primer designated as mBSSP6F2 for RACE
      for mouse BSSP6 (forward)

<400> 27
cttcttttacc cgagctgtgc                                     20

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as mBSSP6F3 to amplify
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<400> 28
taagctagga gaactgaggc                                     20

<210> 29
<211> 18
<212> DNA
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<220>
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<210> 30
<211> 19
<212> DNA
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<220>
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<210> 31
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or mouse BSSP6 (reverse)

<400> 31
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<210> 32
<211> 21
<212> DNA
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<220>
<223> Designed oligonucleotide primer designated as mBSSP6R2 for RACE f
or mouse BSSP6 (reverse)

<400> 32
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<210> 33
<211> 28
<212> DNA
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<220>
<223> Designed oligonucleotide primer designated as mBSSP6R3/E to ampli
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<400> 33
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<210> 34
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer designated as hBSSP6R3 to amplify
a portion of BSSP6 variant type-encoding mRNA from human prostat
ic cancer cell line PC-3 (reverse)

<400> 34
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<210> 35
<211> 20
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<220>

<223> Designed oligonucleotide primer designated as hBSSP6F7 to amplify a portion of human BSSP6-encoding mRNA (forward)

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<210> 36
<211> 20
<212> DNA
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<220>
<223> Designed oligonucleotide primer to amplify conserved region of serin proteases-encoding sequence

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<223> n is a, c, g or t.

<220>
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<223> n is a, c, g or t.

<400> 36
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<210> 37
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<400> 37
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<210> 38
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<220>


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<223>  Designed oligonucleotide to construct plasmid pTrypHis
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tgctgcccc tttcaccate accatcacca tgacgacgat gacaaggatc cgaattc      117

<210>  39
<211>  117
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Designed oligonucleotide to construct plasmid pTrypHis
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gaattcggat ccttgatcatc gtcgtcatgg tgatgggtgat ggtgaaaggg ggcagcaaca      60
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<210>  40
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<212>  PRT
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<220>
<223>  Synthetic

<400>  40
Asp Asp Asp Asp Lys
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<210>  41
<211>  4
<212>  PRT
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<220>
<223>  Synthetic

<400>  41
Lys Val His Gly
1

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